

SEQUENCE LISTING

<110> West, James W.
 Brandt, Cameron S.
 Jaspers, Stephen R.

<120> Production of Homotrimeric Fusion
 Proteins

<130> 02-17

<150> 60/417,801

<151> 2002-10-11

<160> 22

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> C-myc tag.

<400> 1
 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
 1 5 10

<210> 2

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Hemagglutinin A epitope tag

<400> 2
 Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
 1 5

<210> 3

<211> 1377

<212> DNA

<213> Human

<220>

<221> CDS

<222> (14)...(892)

<400> 3
 agcatcctga gta atg agt ggc ctg ggc cgg agc agg cga ggt ggc cgg 49
 Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg
 1 5 10

agc cgt gtg gac cag gag gag cgc ttt cca cag ggc ctg tgg acg ggg 97
 Ser Arg Val Asp Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly
 15 20 25

gtg gct atg aga tcc tgc ccc gaa gag cag tac tgg gat cct ctg ctg 145

Val 30	Ala 30	Met	Arg	Ser	Cys 35	Pro 35	Glu	Glu	Gln	Tyr	Trp 40	Asp	Pro	Leu	Leu	
ggt Gly 45	acc Thr	tgc Cys	atg Met	tcc Ser	tgc Cys 50	aaa Lys	acc Thr	att Ile	tgc Cys	aac Asn 55	cat His	cag Gln	agc Ser	cag Gln	cgc Arg 60	193
acc Thr	tgt Cys	gca Ala	gcc Ala	ttc Phe 65	tgc Cys	agg Arg	tca Ser	ctc Leu	agc Ser 70	tgc Cys	cgc Arg	aag Lys	gag Glu	caa Gln 75	ggc Gly	241
aag Lys	ttc Phe	tat Tyr	gac Asp 80	cat His	ctc Leu	ctg Leu	agg Arg	gac Asp 85	tgc Cys	atc Ile	agc Ser	tgt Cys	gcc Ala 90	tcc Ser	atc Ile	289
tgt Cys	gga Gly	cag Gln 95	cac His	cct Pro	aag Lys	caa Gln	tgt Cys 100	gca Ala	tac Tyr	ttc Phe	tgt Cys	gag Glu 105	aac Asn	aag Lys	ctc Leu	337
agg Arg	agc Ser 110	cca Pro	gtg Val	aac Asn	ctt Leu	cca Pro 115	cca Pro	gag Glu	ctc Leu	agg Arg	aga Arg 120	cag Gln	cgg Arg	agt Ser	gga Gly	385
gaa Glu 125	gtt Val	gaa Glu	aac Asn	aat Asn	tca Ser 130	gac Asp	aac Asn	tcg Ser	gga Gly	agg Arg 135	tac Tyr	caa Gln	gga Gly	ttg Leu	gag Glu 140	433
cac His	aga Arg	ggc Gly	tca Ser	gaa Glu 145	gca Ala	agt Ser	cca Pro	gct Ala	ctc Leu 150	ccg Pro	ggg Gly	ctg Leu	aag Lys	ctg Leu 155	agt Ser	481
gca Ala	gat Asp	cag Gln	gtg Val 160	gcc Ala	ctg Leu	gtc Val	tac Tyr	agc Ser 165	acg Thr	ctg Leu	ggg Gly	ctc Leu	tgc Cys 170	ctg Leu	tgt Cys	529
gcc Ala	gtc Val	ctc Leu 175	tgc Cys	tgc Cys	ttc Phe	ctg Leu	gtg Val 180	gcg Ala	gtg Val	gcc Ala	tgc Cys	ttc Phe 185	ctc Leu	aag Lys	aag Lys	577
agg Arg	ggg Gly 190	gat Asp	ccc Pro	tgc Cys	tcc Ser	tgc Cys 195	cag Gln	ccc Pro	cgc Arg	tca Ser	agg Arg 200	ccc Pro	cgt Arg	caa Gln	agt Ser	625
ccg Pro 205	gcc Ala	aag Lys	tct Ser	tcc Ser	cag Gln 210	gat Asp	cac His	gcg Ala	atg Met	gaa Glu 215	gcc Ala	ggc Gly	agc Ser	cct Pro	gtg Val 220	673
agc Ser	aca Thr	tcc Ser	ccc Pro	gag Glu 225	cca Pro	gtg Val	gag Glu	acc Thr	tgc Cys 230	agc Ser	ttc Phe	tgc Cys	ttc Phe	cct Pro 235	gag Glu	721
tgc Cys	agg Arg	gcg Ala	ccc Pro 240	acg Thr	cag Gln	gag Glu	agc Ser	gca Ala 245	gtc Val	acg Thr	cct Pro	ggg Gly	acc Thr 250	ccc Pro	gac Asp	769
ccc Pro	act Thr	tgt Cys 255	gct Ala	gga Gly	agg Arg	tgg Trp	ggg Gly 260	tgc Cys	cac His	acc Thr	agg Arg	acc Thr 265	aca Thr	gtc Val	ctg Leu	817
cag Gln	cct Pro 270	tgc Cys	cca Pro	cac His	atc Ile	cca Pro 275	gac Asp	agt Ser	ggc Gly	ctt Leu	ggc Gly 280	att Ile	gtg Val	tgt Cys	gtg Val	865

cct gcc cag gag ggg ggc cca ggt gca taaatggggg tcagggaggg 912

Pro Ala Gln Glu Gly Gly Pro Gly Ala
285 290

aaaggaggag ggagagagat ggagaggagg ggagagagaa agagaggtgg ggagagggga 972
gagagatatg aggagagaga gacagaggag gcagaaaggg agagaaacag aggagacaga 1032
gagggagaga gagacagagg gagagagaga cagaggggaa gagaggcaga gagggaaaga 1092
ggcagagaag gaaagagaca ggcagagaag gagagaggca gagagggaga gaggcagaga 1152
gggagagagg cagagagaca gagagggaga gagggacaga gagagataga gcaggaggtc 1212
ggggcactct gagtcccagt tcccagtgca gctgtaggtc gtcacacacct aaccacacgt 1272
gcaataaagt cctcgtgcct gctgctcaca gcccccgaga gcccctcctc ctggagaata 1332
aaacctttgg cagctgcctt tcctcaaaaa aaaaaaaaaa aaaaa 1377

<210> 4
<211> 293
<212> PRT
<213> Human

<400> 4

Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val Asp
1 5 10 15
Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly Val Ala Met Arg
20 25 30
Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met
35 40 45
Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala
50 55 60
Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp
65 70 75 80
His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His
85 90 95
Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val
100 105 110
Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn
115 120 125
Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser
130 135 140
Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val
145 150 155 160
Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val Leu Cys
165 170 175
Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly Asp Pro
180 185 190
Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala Lys Ser
195 200 205
Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr Ser Pro
210 215 220
Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg Ala Pro
225 230 235 240
Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr Cys Ala
245 250 255
Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro Cys Pro
260 265 270
His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro Ala Gln Glu
275 280 285
Gly Gly Pro Gly Ala
290

<210> 5
<211> 21

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> PCR primer

 <400> 5
 gggcctccag gccaccagg t 21

 <210> 6
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PCR primer

 <400> 6
 tcacattgga gccactagga a 21

 <210> 7
 <211> 56
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PCR primer

 <400> 7
 acaggtgtcc aggggaattca tataggccgg ccaccatgga tgcaatgaag agaggg 56

 <210> 8
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PCR primer

 <400> 8
 accctcaggc atcgaacccg aacccgaacc ggatcc 36

 <210> 9
 <211> 118
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PCR primer

 <400> 9
 gatcgatcc atggccgaaa ctgatacctaa aacagttcaa gaccttacca gcgtagtcca 60
 gacgctcctg caagagatcg aagataagtt tcagactatg agcgaccaaa tcattgag 118

 <210> 10
 <211> 100
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PCR primer

<400> 10
 agaatgcatg acatgagctc caggatagat gaccttgaga aaaatatagc agatttaatg 60
 acgcaagctg gtgtggaaga gttggaagga agtggttcta 100

<210> 11
 <211> 110
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 11
 gatctagaac cacttccttc caactcttcc acaccagctt gcgtcattaa atctgctata 60
 tttttctcaa ggcatctat cctggagctc atgtcatcga ttctctcaat 110

<210> 12
 <211> 108
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 12
 gatttggtcg ctcatagtct gaaacttata ttgcatctct tgcaggagcg tctggactac 60
 gctggtaagg tcttgaactg ttttaggata agtttcggcc atggatcc 108

<210> 13
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 13
 cacacgtacg aagatggatg caatgaagag agg 33

<210> 14
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 14
 ggttagatct cgaacccgaa cccgaaccgg 30

<210> 15
 <211> 62
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 15
 ctagaaataa ttttgtttta ctttaagaag gagatatata tatggctatg agatcctgcc 60
 cc 62

<210> 16
 <211> 64
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 16
 tctgtatcag gctgaaaatc ttatctcatc cgccaaaaca ctagtgatgg tgatggatgat 60
 ggcc 64

<210> 17
 <211> 516
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TACI-HSBP fragment

<400> 17
 atggctatga gatcctgccc cgaagagcag tactgggcatc ctctgctggg tacctgcatg 60
 tcctgcaaaa ccatttgcaa ccatcagagc cagcgcacct gtgcagcctt ctgcagggtca 120
 ctcagctgcc gcaaggagca aggcaagttc tatgaccatc tcctgaggga ctgcatcagc 180
 tgtgcctcca tctgtggaca gcaccctaag caatgtgcat acttctgtga gaacaagctc 240
 aggagcggat ccggttcggg ttcgggttcg agatccatgg ccgaaactga tcctaaaaca 300
 gttcaagacc ttaccagcgt agtccagacg ctctgcaag agatgcaaga taagtttcag 360
 actatgagcg accaaatcat tgagagaatc gatgacatga gctccaggat agatgacctt 420
 gagaaaaata tagcagattt aatgacgcaa gctgggtgtgg aagagttgga aggaagtgg 480
 tctagatccg gtggccatca ccatcaccat cactga 516

<210> 18
 <211> 171
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TACI-HSBP fragment

<400> 18
 Met Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
 1 5 10 15
 Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
 20 25 30
 Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
 35 40 45
 Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
 50 55 60
 Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
 65 70 75 80
 Arg Ser Gly Ser Gly Ser Gly Ser Gly Ser Arg Ser Met Ala Glu Thr
 85 90 95
 Asp Pro Lys Thr Val Gln Asp Leu Thr Ser Val Val Gln Thr Leu Leu
 100 105 110
 Gln Glu Met Gln Asp Lys Phe Gln Thr Met Ser Asp Gln Ile Ile Glu
 115 120 125
 Arg Ile Asp Asp Met Ser Ser Arg Ile Asp Asp Leu Glu Lys Asn Ile
 130 135 140
 Ala Asp Leu Met Thr Gln Ala Gly Val Glu Glu Leu Glu Gly Ser Gly
 145 150 155 160
 Ser Arg Ser Gly Gly His His His His His His
 165 170

<210> 19
 <211> 480
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> NC-1 fragment

<221> CDS
 <222> (1)...(480)

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<400> 19
atg cct gag ggt ttt ata aag gca ggc caa agg ccc agt ctt tct ggg      48
Met Pro Glu Gly Phe Ile Lys Ala Gly Gln Arg Pro Ser Leu Ser Gly
  1          5          10          15

acc cct ctt gtt agt gcc aac cag cgg gta aca gga atg cct gtg tct      96
Thr Pro Leu Val Ser Ala Asn Gln Arg Val Thr Gly Met Pro Val Ser
          20          25          30

gct ttt act gtt att ctc tcc aaa gct tac cca gca ata gga act ccc      144
Ala Phe Thr Val Ile Leu Ser Lys Ala Tyr Pro Ala Ile Gly Thr Pro
          35          40          45

ata cca ttt gat aaa att ttg tat aac agg caa cag cat tat gac cca      192
Ile Pro Phe Asp Lys Ile Leu Tyr Asn Arg Gln Gln His Tyr Asp Pro
          50          55          60

agg act gga atc ttt act tgt cag ata cca gga ata tac tat ttt tca      240
Arg Thr Gly Ile Phe Thr Cys Gln Ile Pro Gly Ile Tyr Tyr Phe Ser
          65          70          75          80

tac cac gtg cat gtg aaa ggg act cat gtt tgg gta ggc ctg tat aag      288
Tyr His Val His Val Lys Gly Thr His Val Trp Val Gly Leu Tyr Lys
          85          90          95

aat ggc acc cct gta atg tac acc tat gat gaa tac acc aaa ggc tac      336
Asn Gly Thr Pro Val Met Tyr Thr Tyr Asp Glu Tyr Thr Lys Gly Tyr
          100          105          110

ctg gat cag gct tca ggg agt gcc atc atc gat ctc aca gaa aat gac      384
Leu Asp Gln Ala Ser Gly Ser Ala Ile Ile Asp Leu Thr Glu Asn Asp
          115          120          125

cag gtg tgg ctc cag ctt ccc aat gcc gag tca aat ggc cta tac tcc      432
Gln Val Trp Leu Gln Leu Pro Asn Ala Glu Ser Asn Gly Leu Tyr Ser
          130          135          140

tct gag tat gtc cac tcc tct ttc tca gga ttc cta gtg gct cca atg      480
Ser Glu Tyr Val His Ser Ser Phe Ser Gly Phe Leu Val Ala Pro Met
          145          150          155          160

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<210> 20
 <211> 160
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> NC-1 fragment

<400> 20

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Met Pro Glu Gly Phe Ile Lys Ala Gly Gln Arg Pro Ser Leu Ser Gly
 1      5      10      15
Thr Pro Leu Val Ser Ala Asn Gln Arg Val Thr Gly Met Pro Val Ser
      20      25      30
Ala Phe Thr Val Ile Leu Ser Lys Ala Tyr Pro Ala Ile Gly Thr Pro
      35      40      45
Ile Pro Phe Asp Lys Ile Leu Tyr Asn Arg Gln Gln His Tyr Asp Pro
      50      55      60
Arg Thr Gly Ile Phe Thr Cys Gln Ile Pro Gly Ile Tyr Tyr Phe Ser
      65      70      75      80
Tyr His Val His Val Lys Gly Thr His Val Trp Val Gly Leu Tyr Lys
      85      90      95
Asn Gly Thr Pro Val Met Tyr Thr Tyr Asp Glu Tyr Thr Lys Gly Tyr
      100      105      110
Leu Asp Gln Ala Ser Gly Ser Ala Ile Ile Asp Leu Thr Glu Asn Asp
      115      120      125
Gln Val Trp Leu Gln Leu Pro Asn Ala Glu Ser Asn Gly Leu Tyr Ser
      130      135      140
Ser Glu Tyr Val His Ser Ser Phe Ser Gly Phe Leu Val Ala Pro Met
145      150      155      160

```

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<210> 21
<211> 195
<212> DNA
<213> Artificial Sequence

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<220>
<223> HSBP-1 fragment

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<221> CDS
<222> (1)...(195)

```

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<400> 21
atg gcc gaa act gat cct aaa aca gtt caa gac ctt acc agc gta gtc      48
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 1      5      10      15

cag acg ctc ctg caa gag atg caa gat aag ttt cag act atg agc gac      96
Gln Thr Leu Leu Gln Glu Met Gln Asp Lys Phe Gln Thr Met Ser Asp
      20      25      30

caa atc att gag aga atc gat gac atg agc tcc agg ata gat gac ctt      144
Gln Ile Ile Glu Arg Ile Asp Asp Met Ser Ser Arg Ile Asp Asp Leu
      35      40      45

gag aaa aat ata gca gat tta atg acg caa gct ggt gtg gaa gag ttg      192
Glu Lys Asn Ile Ala Asp Leu Met Thr Gln Ala Gly Val Glu Glu Leu
      50      55      60

gaa      195

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<210> 22
<211> 65
<212> PRT
<213> Artificial Sequence

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<220>
<223> HSBP-1 fragment

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      <400> 22
Met  Ala  Glu  Thr  Asp  Pro  Lys  Thr  Val  Gln  Asp  Leu  Thr  Ser  Val  Val
 1          5          10          15
Gln  Thr  Leu  Leu  Gln  Glu  Met  Gln  Asp  Lys  Phe  Gln  Thr  Met  Ser  Asp
      20          25          30
Gln  Ile  Ile  Glu  Arg  Ile  Asp  Asp  Met  Ser  Ser  Arg  Ile  Asp  Asp  Leu
      35          40          45
Glu  Lys  Asn  Ile  Ala  Asp  Leu  Met  Thr  Gln  Ala  Gly  Val  Glu  Glu  Leu
      50          55          60
Glu
65

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